

SEQUENCE

SEQ ID NO: 1

Sequence Length: 780

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: cDNA

Sequence

TTGGTGAAGCT CTAAACGGCTG TTTTGACTGG CGTAGCCGGA GCCGGCGACG TGAGGCGGGC 60  
GTTGCTCGCG CGACAAGTAG TTGCTGGGAC AGCGAA ATG GAG GGG TGT GTG TCT 114  
Met Glu Gly Cys Val Ser  
1 5  
AAC CTA ATG GTC TGC AAC CTG GCC TAC AGC GGG AAG CTG GAA GAG TTG 162  
Asn Leu Met Val Cys Asn Leu Ala Tyr Ser Gly Lys Leu Glu Glu Leu  
10 15 20  
AAG GAG AGT ATT CTG GCC GAT AAA TCC CTG GCT ACT AGA ACT GAC CAG 210  
Lys Glu Ser Ile Leu Ala Asp Lys Ser Leu Ala Thr Arg Thr Asp Gln  
25 30 35  
GAC AGC AGA ACT GCA TTG CAC TGG GCA TGC TCA GCT GGA CAT ACA GAA 258  
Asp Ser Arg Thr Ala Leu His Trp Ala Cys Ser Ala Gly His Thr Glu  
40 45 50  
ATT GTT GAA TTT TTG TTG CAA CTT GGA GTG CCA GTG AAT GAT AAA GAC 306  
Ile Val Glu Phe Leu Leu Gln Leu Gly Val Pro Val Asn Asp Lys Asp  
55 60 65 70  
GAT GCA GGT TGG TCT CCT CTT CAT ATT GCG GCT TCT GCT GGC CGG GAT 354  
Asp Ala Gly Trp Ser Pro Leu His Ile Ala Ala Ser Ala Gly Arg Asp  
75 80 85  
GAG ATT GTA AAA GCC CTT CTG GGA AAA GGT GCT CAA GTG AAT GCT GTC 402  
Glu Ile Val Lys Ala Leu Leu Gly Lys Gly Ala Gln Val Asn Ala Val  
90 95 100  
AAT CAA AAT GGC TGT ACT CCC TTA CAT TAT GCA GCT TCG AAA AAC AGG 450  
Asn Gln Asn Gly Cys Thr Pro Leu His Tyr Ala Ala Ser Lys Asn Arg  
105 110 115  
CAT GAG ATC GCT GTC ATG TTA CTG GAA GGC GGG GCT AAT CCA GAT GCT 498  
His Glu Ile Ala Val Met Leu Leu Glu Gly Gly Ala Asn Pro Asp Ala  
120 125 130

001105560560

SEQ ID NO: 2  
Sequence Length: 226  
Sequence Type: Amino acid  
Topology: Linear  
Molecular Type: Protein

Met	Glu	Gly	Cys	Val	Ser	Asn	Leu	Met	Val	Cys	Asn	Leu	Ala	Tyr	Ser
1				5					10					15	
Gly	Lys	Leu	Glu	Glu	Leu	Lys	Glu	Ser	Ile	Leu	Ala	Asp	Lys	Ser	Leu
			20					25					30		
Ala	Thr	Arg	Thr	Asp	Gln	Asp	Ser	Arg	Thr	Ala	Leu	His	Trp	Ala	Cys
		35					40					45			
Ser	Ala	Gly	His	Thr	Glu	Ile	Val	Glu	Phe	Leu	Leu	Gln	Leu	Gly	Val
	50					55					60				
Pro	Val	Asn	Asp	Lys	Asp	Asp	Ala	Gly	Trp	Ser	Pro	Leu	His	Ile	Ala
65				70						75					80
Ala	Ser	Ala	Gly	Arg	Asp	Glu	Ile	Val	Lys	Ala	Leu	Leu	Gly	Lys	Gly
			85						90					95	
Ala	Gln	Val	Asn	Ala	Val	Asn	Gln	Asn	Gly	Cys	Thr	Pro	Leu	His	Tyr
			100						105				110		

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SEQ ID NO: 3
Sequence Length: 693
Sequence Type: Nucleic acid
Strandedness: Double
Topology: Linear
Molecular Type: cDNA
Sequence
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ATG	GAG	GGG	TGT	GTG	TCT	AAC	ATA	ATG	ATC	TGT	AAC	CTG	GCC	TAC	AGT	48
Met	Glu	Gly	Cys	Val	Ser	Asn	Ile	Met	Ile	Cys	Asn	Leu	Ala	Tyr	Ser	
5					10					15						
GGG	AAG	CTG	GAT	GAG	TTG	AAG	GAG	CGC	ATT	TTG	GCT	GAT	AAA	TCT	CTG	96
Gly	Lys	Leu	Asp	Glu	Leu	Lys	Glu	Arg	Ile	Leu	Ala	Asp	Lys	Ser	Leu	
20					25					30						
GCT	ACT	AGA	ACT	GAT	CAG	GAC	AGC	AGA	ACA	GCT	TTG	CAC	TGG	GCA	TGC	144
Ala	Thr	Arg	Thr	Asp	Gln	Asp	Ser	Arg	Thr	Ala	Leu	His	Trp	Ala	Cys	
35					40					45						
TCA	GCT	GGC	CAT	ACA	GAA	ATT	GTT	GAA	TTC	TTG	CTG	CAA	CTT	GGA	GTG	192
Ser	Ala	Gly	His	Thr	Glu	Ile	Val	Glu	Phe	Leu	Leu	Gln	Leu	Gly	Val	
50					55					60						

SEQ ID NO: 4  
Sequence Length: 231  
Sequence Type: Amino acid  
Topology: Linear  
Molecular Type: Protein

[illegible]

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SEQ ID NO: 5
Sequence Length: 693
Sequence Type: Nucleic acid
Strandedness: Double
Topology: Linear
Molecular Type: cDNA

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Sequence

ATG GAG GGG TGT GTG TCT AAC CTA ATG GTC TGT AAC CTG GCC TAC AAC	48
Met Glu Gly Cys Val Ser Asn Leu Met Val Cys Asn Leu Ala Tyr Asn	
5 10 15	
GGG AAG CTG GAT GAG TTG AAG GAA AGC ATT TTG GCT GAT AAG TCT CTG	96
Gly Lys Leu Asp Glu Leu Lys Glu Ser Ile Leu Ala Asp Lys Ser Leu	
20 25 30	
GCC ACT AGA ACT GAT CAG GAC AGC AGA ACA GCA TTG CAC TGG GCA TGC	144
Ala Thr Arg Thr Asp Gln Asp Ser Arg Thr Ala Leu His Trp Ala Cys	
35 40 45	
TCA GCT GGT CAT ACA GAA ATT GTT GAA TTC TTG CTG CAA CTT GGA GTG	192
Ser Ala Gly His Thr Glu Ile Val Glu Phe Leu Leu Gln Leu Gly Val	
50 55 60	
CCA GTA AAT GAA AAA GAC GAT GCA GGT TGG TCT CCT CTT CAT ATT GCT	240
Pro Val Asn Glu Lys Asp Asp Ala Gly Trp Ser Pro Leu His Ile Ala	
65 70 75 80	
GCT TCC GCT GGC CGG GAT GAG ATT GTA AAA GCC CTT CTG ATA AAA GGG	288
Ala Ser Ala Gly Arg Asp Glu Ile Val Lys Ala Leu Leu Ile Lys Gly	
85 90 95	
GCA CAA GTG AAT GCC GTC AAT CAG AAT GGC TGC ACG GCC CTT CAT TAT	336
Ala Gln Val Asp Ala Val Asn Gln Asn Gly Cys Thr Ala Leu His Tyr	
100 105 110	
GCA GCT TCC AAG AAT AGG CAT GAG ATT GCT GTT ATG TTA CTA GAA GGT	384
Ala Ala Ser Lys Asn Arg His Glu Ile Ala Val Met Leu Leu Glu Gly	
115 120 125	
GGG GCT AAT CCA GAT GCT AAG AAC CAT TAT GAT GCT ACA GCA ATG CAC	432
Gly Ala Asn Pro Asp Ala Lys Asn His Tyr Asp Ala Thr Ala Met His	
130 135 140	
CGG GCA GCA GCC AAG GGT AAC TTG AAG ATG GTT CAT ATC CTT CTG TTC	480
Arg Ala Ala Ala Lys Gly Asn Leu Lys Met Val His Ile Leu Leu Phe	
145 150 155 160	
TAC AAA GCA TCC ACA AAC ATC CAA GAT ACT GAG GGT AAC ACT CCT CTA	528
Tyr Lys Ala Ser Thr Asn Ile Gln Asp Thr Glu Gly Asn Thr Pro Leu	
165 170 175	
CAC TTA GCC TGT GAT GAG GAG AGA GTG GAA GAA GCA AAA TTG CTG GTG	576
His Leu Ala Cys Asp Glu Glu Arg Val Glu Glu Ala Lys Leu Leu Val	
180 185 190	

0050975-033100

ACC CAA GGA GCA AGT ATT TAC ATT GAA AAT AAG GAA GAA AAG ACA CCG 624  
 Thr Gln Gly Ala Ser Ile Tyr Ile Glu Asn Lys Glu Glu Lys Thr Pro  
 195 200 205  
 CTG CAA GTC GCG AAA GGG GGC CTG GGT TTA ATA CTC AAA AGA ATC GCA 672  
 Leu Gln Val Ala Lys Gly Gly Leu Gly Leu Ile Leu Lys Arg Ile Ala  
 210 215 220  
 GAA AGT GAA GAG GCT TCT ATG TAG 720  
 Glu Ser Glu Glu Ala Ser Met  
 225 230

SEQ ID NO: 6  
 Sequence Length: 231  
 Sequence Type: Amino acid  
 Topology: Linear  
 Molecular Type: Protein  
 Sequence

Met Glu Gly Cys Val Ser Asn Leu Met Val Cys Asn Leu Ala Tyr Asn  
 1 5 10 15  
 Gly Lys Leu Asp Glu Leu Lys Glu Ser Ile Leu Ala Asp Lys Ser Leu  
 20 25 30  
 Ala Thr Arg Thr Asp Gln Asp Ser Arg Thr Ala Leu His Trp Ala Cys  
 35 40 45  
 Ser Ala Gly His Thr Glu Ile Val Glu Phe Leu Leu Gln Leu Gly Val  
 50 55 60  
 Pro Val Asn Glu Lys Asp Asp Ala Gly Trp Ser Pro Leu His Ile Ala  
 65 70 75 80  
 Ala Ser Ala Gly Arg Asp Glu Ile Val Lys Ala Leu Leu Ile Lys Gly  
 85 90 95  
 Ala Gln Val Asn Ala Val Asn Gln Asn Gly Cys Thr Ala Leu His Tyr  
 100 105 110  
 Ala Ala Ser Lys Asn Arg His Glu Ile Ala Val Met Leu Leu Glu Gly  
 115 120 125  
 Gly Ala Asn Pro Asp Ala Lys Asn His Tyr Asp Ala Thr Ala Met His  
 130 135 140  
 Arg Ala Ala Ala Lys Gly Asn Leu Lys Met Val His Ile Leu Leu Phe  
 145 150 155 160  
 Tyr Lys Ala Ser Thr Asn Ile Gln Asp Thr Glu Gly Asn Thr Pro Leu  
 165 170 175

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